



Exhibit 1

- X - 82

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- T830X
- (i) APPLICANTS: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.
- (ii) TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
- (iii) NUMBER OF SEQUENCES: 43
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORGAN & FINNEGAN
(B) STREET: 345 PARK AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/231,565
(B) FILING DATE: 22-APR-1994
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: CAROL M. GRUPPI
(B) REGISTRATION NUMBER: 37,341
(C) REFERENCE/DOCKET NUMBER: 2026-4124
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 758-4800
(B) TELEFAX: (212) 751-6849
(C) TELEX: 421792
- B'

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1559
(B) TYPE: NUCLEOTIDE
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN
- (ii) MOLECULE TYPE: cDNA
- 83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCAGACAGA	GGACTCTCAT	TAAGGAAGGT	GTCCTGTGCC	40
CTGACCCTAC	AAGATGCCAA	GAGAAGATGC	TCACTTCATC	80
TATGGTTACC	CCAAGAAGGG	GCACGGCCAC	TCTTACACCA	120
CGGCTGAAGA	GGCCGCTGGG	ATCGGCATCC	TGACAGTGAT	160
CCTGGGAGTC	TTACTGCTCA	TCGGCTGTTG	GTATTGTAGA	200
AGACGAAATG	GATACAGAGC	CTTGATGGAT	AAAAGTCTTC	240
ATGTTGGCAC	TCAATGTGCC	TTAACAAGAA	GATGCCCACA	280
AGAAGGGTTT	GATCATCGGG	ACAGCAAAGT	GTCTCTTCAA	320
GAGAAAAACT	GTGAACCTGT	GGTCCCAAT	GCTCCACCTG	360
CTTATGAGAA	ACTCTCTGCA	GAACAGTCAC	CACCACCTTA	400
TTCACCTTAA	GAGCCAGCGA	GACACCTGAG	ACATGCTGAA	440
ATTATTTCTC	TCACACTTTT	GCTTGAATTT	AATACAGACA	480
TCTAATGTTT	TCCTTTGGAA	TGGTGTAGGA	AAAATGCAAG	520
CCATCTCTAA	TAATAAGTCA	GTGTTAAAAT	TTTAGTAGGT	560
CCGCTAGCAG	TACTAATCAT	GTGAGGAAAT	GATGAGAAAT	600
ATTAAATTGG	GAAAACTCCA	TCAATAAATG	TTGCAATGCA	640
TGATACTATC	TGTGCCAGAG	GTAATGTTAG	TAAATCCATG	680
GTGTTATTTT	CTGAGAGACA	GAATTCAAGT	GGGTATTCTG	720
GGGCCATCCA	ATTTCTCTTT	ACTTGAAATT	TGGCTAATAA	760
CAAAC TAGTC	AGGTTTTTCGA	ACCTTGACCG	ACATGAACTG	800
TACACAGAAT	TGTTCCAGTA	CTATGGAGTG	CTCACAAAGG	840
ATACTTTTAC	AGGTTAAGAC	AAAGGGTTGA	CTGGCCTATT	880
TATCTGATCA	AGAACATGTC	AGCAATGTCT	CTTTGTGCTC	920
TAAAATTCTA	TTATACTACA	ATAATATATT	GTAAAGATCC	960

B'
Cont.

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B' Cmt.

TATAGCTCTT TTTTTTTGAG ATGGAGTTTC GCTTTTGTTC	1000
CCCAGGCTGG AGTGCAATGG CGCGATCTTG GCTCACCATA	1040
ACCTCCGCCT CCCAGGTTCA AGCAATTCTC CTGCCTTAGC	1080
CTCCTGAGTA GCTGGGATTA CAGGCGTGCG CCACTATGCC	1120
TGACTAATTT TGTAGTTTTA GTAGAGACGG GGTTCCTCCA	1160
TGTTGGTCAG GCTGGTCTCA AACTCCTGAC CTCAGGTGAT	1200
CTGCCCCGCT CAGCCTCCCA AAGTGCTGGA ATTACAGGCG	1240
TGAGCCACCA CGCCTGGCTG GATCCTATAT CTTAGGTAAG	1280
ACATATAACG CAGTCTAATT ACATTTCACT TCAAGGCTCA	1320
ATGCTATTCT AACTAATGAC AAGTATTTTC TACTAAACCA	1360
GAAATTGGTA GAAGGATTTA AATAAGTAAA AGCTACTATG	1400
TACTGCCTTA GTGCTGATGC CTGTGTACTG CCTTAAATGT	1440
ACCTATGGCA ATTTAGCTCT CTTGGGTTCC CAAATCCCTC	1480
TCACAAGAAT GTGCAGAAGA AATCATAAAG GATCAGAGAT	1520
TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1559

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Arg	Glu	Asp	Ala	His	Phe	Ile	Tyr	Gly	Tyr	Pro	Lys
1				5						10			
Lys	Gly	His	Gly	His	Ser	Tyr	Thr	Thr	Ala	Glu	Glu	Ala	Ala
15					20					25			

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Gly Ile Gly Ile Leu Thr Val Ile Leu Gly Val Leu Leu Leu
30 35 40
Ile Gly Cys Trp Tyr Cys Arg Arg Arg Asn Gly Tyr Arg Ala
45 50 55
Leu Met Asp Lys Ser Leu His Val Gly Thr Gln Cys Ala Leu
60 65 70
Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp His Arg Asp Ser
75 80
Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val Val Pro
85 90 95
Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser
100 105 110
Pro Pro Pro Tyr Ser Pro
115

B
Cont.

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: Unknown
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Thr Ala Glu Glu Ala Ala Gly Ile
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: Unknown
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Ala Ala Gly Ile Gly Ile Leu Thr Val
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: Unknown
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

B'
cont.

Gly Ile Gly Ile Leu Thr Val Ile Leu
1 5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: Unknown
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Ile Leu Thr Val Ile Leu Gly Val
1 5

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: Unknown
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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Ile Leu Thr Val Ile Leu Gly Val Leu
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Thr Val Ile Leu Gly Val Leu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Val Ile Leu Gly Val Leu Leu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Val Ile Leu Gly Val Leu Leu Ile
1 5

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

B1
Cont.

Ala Leu Met Asp Lys Ser Leu His Val
1 5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Leu His Val Gly Thr Gln Cys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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Pro Val Val Pro Asn Ala Pro Pro Ala
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Ala Pro Pro Ala Tyr Glu Lys Leu
1 5

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr Thr Thr Ala Glu Glu Ala Ala Gly Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

90
- 8 -

Thr Ala Glu Glu Ala Ala Gly Ile Gly Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

B
Cmt-
Glu Ala Ala Gly Ile Gly Ile Leu Thr Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Ala Gly Ile Gly Ile Leu Thr Val Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gly Ile Leu Thr Val Ile Leu Gly Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile Leu Thr Val Ile Leu Gly Val Leu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Leu Thr Val Ile Leu Gly Val Leu Leu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Thr Val Ile Leu Gly Val Leu Leu Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: Unknown
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

B' Cnt.
Arg Ala Leu Met Asp Lys Ser Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: Unknown
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Leu His Val Gly Thr Gln Cys Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: Unknown
 - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ser Leu Gln Glu Lys Asn Cys Glu Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2172
(B) TYPE: nucleotide
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

B' Cont.

GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT	40
GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG	80
ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA	120
GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC	160
CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA	200
GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC	240
TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA	280
TGCCTCCTTC TCTATTGCCT TGAACCTCCC TGGAAGCCAA	320
AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA	360
CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT	400
GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT	440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA	480
GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA	520
ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA	560
GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGACTG	600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC	640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT	680

B
Cont.

TTCTCCGTGA	GCGTGTCCCA	GTTGCGGGCC	TTGGATGGAG	720
GGAACAAGCA	CTTCCTGAGA	AATCAGCCTC	TGACCTTTGC	760
CCTCCAGCTC	CATGACCCCA	GTGGCTATCT	GGCTGAAGCT	800
GACCTCTCCT	ACACCTGGGA	CTTTGGAGAC	AGTAGTGGAA	840
CCCTGATCTC	TCGGGCACTT	GTGGTCACTC	ATACTTACCT	880
GGAGCCTGGC	CCAGTCACTG	CCCAGGTGGT	CCTGCAGGCT	920
GCCATTCCTC	TCACCTCCTG	TGGCTCCTCC	CCAGTTCCAG	960
GCACCACAGA	TGGGCACAGG	CCAAGTGCAG	AGGCCCTTAA	1000
CACCACAGCT	GGCCAAGTGC	CTACTACAGA	AGTTGTGGGT	1040
ACTACACCTG	GTCAGGCGCC	AACTGCAGAG	CCCTCTGGAA	1080
CCACATCTGT	GCAGGTGCCA	ACCACTGAAG	TCATAAGCAC	1120
TGCACCTGTG	CAGATGCCAA	CTGCAGAGAG	CACAGGTATG	1160
ACACCTGAGA	AGGTGCCAGT	TTCAGAGGTC	ATGGGTACCA	1200
CACTGGCAGA	GATGTCAACT	CCAGAGGCTA	CAGGTATGAC	1240
ACCTGCAGAG	GTATCAATTG	TGGTGCTTTC	TGGAACCACA	1280
GCTGCACAGG	TAACAACCTAC	AGAGTGGGTG	GAGACCACAG	1320
CTAGAGAGCT	ACCTATCCCT	GAGCCTGAAG	GTCCAGATGC	1360
CAGCTCAATC	ATGTCTACGG	AAAGTATTAC	AGGTTCCCTG	1400
GGCCCCCTGC	TGGATGGTAC	AGCCACCTTA	AGGCTGGTGA	1440
AGAGACAAGT	CCCCCTGGAT	TGTGTTCTGT	ATCGATATGG	1480
TTCCTTTTCC	GTCACCCTGG	ACATTGTCCA	GGGTATTGAA	1520
AGTGCCGAGA	TCCTGCAGGC	TGTGCCGTCC	GGTGAGGGGG	1560
ATGCATTTGA	GCTGACTGTG	TCCTGCCAAG	GCGGGCTGCC	1600
CAAGGAAGCC	TGCATGGAGA	TCTCATCGCC	AGGGTGCCAG	1640
CCCCCTGCCC	AGCGGCTGTG	CCAGCCTGTG	CTACCCAGCC	1680

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B' cont.

CAGCCTGCCA GCTGGTCTCTG CACCAGATAC TGAAGGGTGG	1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC	1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG	1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG	1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG	1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC	1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TCGTCTACC	1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC	2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG	2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTC	2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT	2120
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA	2160
AAAAAAAAAA AA	2172

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Asp	Leu	Val	Leu	Lys	Arg	Cys	Leu	Leu	His	Leu
1				5						10	

Ala	Val	Ile	Gly	Ala	Leu	Leu	Ala	Val	Gly	Ala	Thr
		15					20				
Lys	Val	Pro	Arg	Asn	Gln	Asp	Trp	Leu	Gly	Val	Ser
25					30					35	
Arg	Gln	Leu	Arg	Thr	Lys	Ala	Trp	Asn	Arg	Gln	Leu
			40					45			
Tyr	Pro	Glu	Trp	Thr	Glu	Ala	Gln	Arg	Leu	Asp	Cys
	50					55				60	
Trp	Arg	Gly	Gly	Gln	Val	Ser	Leu	Lys	Val	Ser	Asn
				65					70		
Asp	Gly	Pro	Thr	Leu	Ile	Gly	Ala	Asn	Ala	Ser	Phe
		75					80				
Ser	Ile	Ala	Leu	Asn	Phe	Pro	Gly	Ser	Gln	Lys	Val
85					90					95	
Leu	Pro	Asp	Gly	Gln	Val	Ile	Trp	Val	Asn	Asn	Thr
			100					105			
Ile	Ile	Asn	Gly	Ser	Gln	Val	Trp	Gly	Gly	Gln	Pro
	110					115					120
Val	Tyr	Pro	Gln	Glu	Thr	Asp	Asp	Ala	Cys	Ile	Phe
				125					130		
Pro	Asp	Gly	Gly	Pro	Cys	Pro	Ser	Gly	Ser	Trp	Ser
		135					140				
Gln	Lys	Arg	Ser	Phe	Val	Tyr	Val	Trp	Lys	Thr	Trp
145					150					155	
Gly	Gln	Tyr	Trp	Gln	Phe	Leu	Gly	Gly	Pro	Val	Ser
			160					165			
Gly	Leu	Ser	Ile	Gly	Thr	Gly	Arg	Ala	Met	Leu	Gly
	170					175					180
Thr	His	Thr	Met	Glu	Val	Thr	Val	Tyr	His	Arg	Arg
				185					190		
Gly	Ser	Arg	Ser	Tyr	Val	Pro	Leu	Ala	His	Ser	Ser
		195					200				
Ser	Ala	Phe	Thr	Ile	Thr	Asp	Gln	Val	Pro	Phe	Ser
205					210					215	
Val	Ser	Val	Ser	Gln	Leu	Arg	Ala	Leu	Asp	Gly	Gly
			220					225			
Asn	Lys	His	Phe	Leu	Arg	Asn	Gln	Pro	Leu	Thr	Phe
	230					235					240
Ala	Leu	Gln	Leu	His	Asp	Pro	Ser	Gly	Tyr	Leu	Ala
				245					250		
Glu	Ala	Asp	Leu	Ser	Tyr	Thr	Trp	Asp	Phe	Gly	Asp
		255					260				
Ser	Ser	Gly	Thr	Leu	Ile	Ser	Arg	Ala	Leu	Val	Val
260					265					270	
Thr	His	Thr	Tyr	Leu	Glu	Pro	Gly	Pro	Val	Thr	Ala
			275					280			
Gln	Val	Val	Leu	Gln	Ala	Ala	Ile	Pro	Leu	Thr	Ser
	285					290					295
Cys	Gly	Ser	Ser	Pro	Val	Pro	Gly	Thr	Thr	Asp	Gly
				300					305		
His	Arg	Pro	Thr	Ala	Glu	Ala	Pro	Asn	Thr	Thr	Ala
		310					315				

B'
Cont.

Gly Gln Val Pro Thr Thr Glu Val Val Gly Thr Thr
320 325 330
Pro Gly Gln Ala Pro Thr Ala Glu Pro Ser Gly Thr
335 340
Thr Ser Val Gln Val Pro Thr Thr Glu Val Ile Ser
345 350 355
Thr Ala Pro Val Gln Met Pro Thr Ala Glu Ser Thr
360 365
Gly Met Thr Pro Glu Lys Val Pro Val Ser Glu Val
370 375
Met Gly Thr Thr Leu Ala Glu Met Ser Thr Pro Glu
380 385 390
Ala Thr Gly Met Thr Pro Ala Glu Val Ser Ile Val
395 400
Val Leu Ser Gly Thr Thr Ala Ala Gln Val Thr Thr
405 410 415
Thr Glu Trp Val Glu Thr Thr Ala Arg Glu Leu Pro
420 425
Ile Pro Glu Pro Glu Gly Pro Asp Ala Ser Ser Ile
430 435
Met Ser Thr Glu Ser Ile Thr Gly Ser Leu Gly Pro
440 445 450
Leu Leu Asp Gly Thr Ala Thr Leu Arg Leu Val Lys
455 460
Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr
465 470 475
Gly Ser Phe Ser Val Thr Leu Asp Ile Val Gln Gly
480 490
Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Pro Ser
495 500
Gly Glu Gly Asp Ala Phe Glu Leu Thr Val Ser Cys
505 510 515
Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Glu Ile
520 525
Ser Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu
530 535 540
Cys Gln Pro Val Leu Pro Ser Pro Ala Cys Gln Leu
545 550
Val Leu His Gln Ile Leu Lys Gly Gly Ser Gly Thr
555 560
Tyr Cys Leu Asn Val Ser Leu Ala Asp Thr Asn Ser
565 570 575
Leu Ala Val Val Ser Thr Gln Leu Ile Met Pro Gly
580 585
Gln Glu Ala Gly Leu Gly Gln Val Pro Leu Ile Val
590 595 600
Gly Ile Leu Leu Val Leu Met Ala Val Val Leu Ala
605 610
Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys Gln Asp
615 620

B'
Cont.

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- 27 -

Phe Ser Val Pro Gln Leu Pro His Ser Ser Ser His
625 630 635
Trp Leu Arg Leu Pro Arg Ile Phe Cys Ser Cys Pro
640 645
Ile Gly Glu Asn Ser Pro Leu Leu Ser Gly Gln Gln
650 655 660
Val

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Val Pro Gly Ile Leu Leu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Leu Leu Ser Gly Gln Gln Val
1 5

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Pro Pro Gln Trp Ala Ala Gly Leu Ser Thr Leu Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu Leu Asp Gly Thr Ala Thr Leu Arg Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Val Leu Tyr Arg Tyr Gly Ser Phe Ser Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ala Leu Asp Gly Gly Asn Lys His Phe Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Val Leu Lys Arg Cys Leu Leu His Leu
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Val Leu Pro Ser Pro Ala Cys Gln Leu Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Leu Ala Asp Thr Asn Ser Leu Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ser Val Ser Val Ser Gln Leu Arg Ala
1 5

B' cont.
(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Tyr Leu Glu Pro Gly Pro Val Thr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Leu Asn Val Ser Leu Ala Asp Thr Asn
1 5

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5
